

Figure 1A

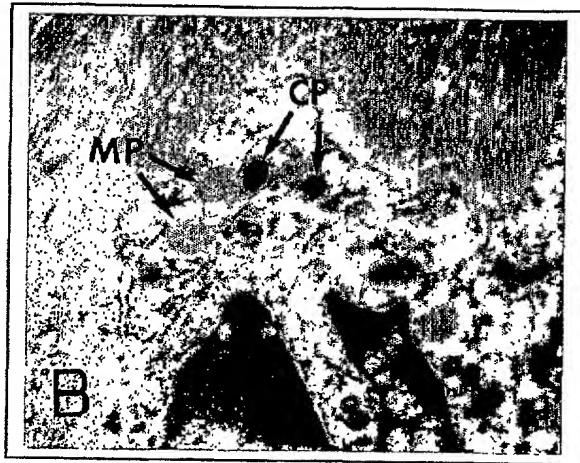


Figure 1B

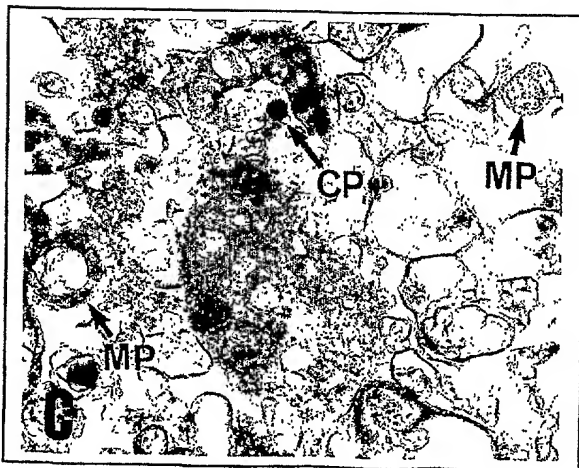


Figure 1C

201000 5169800F

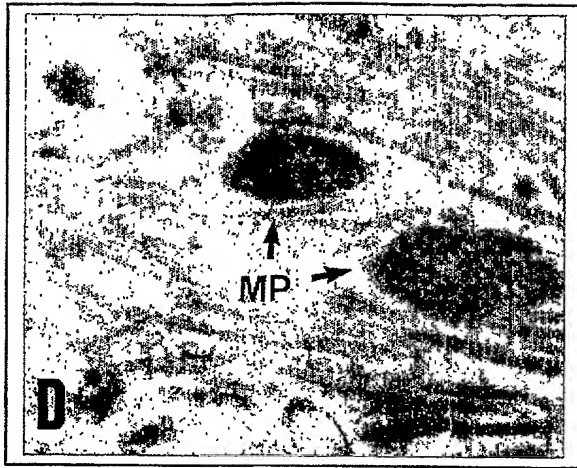


Figure 1D

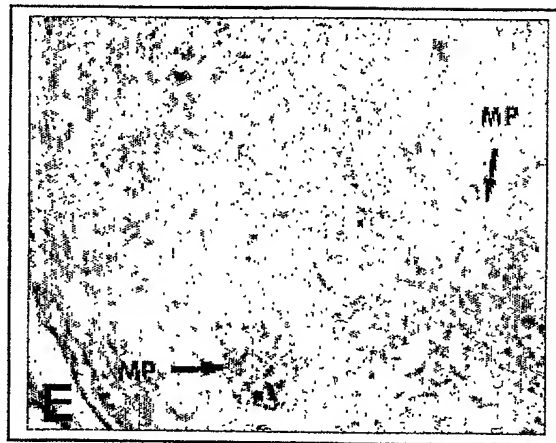


Figure 1E

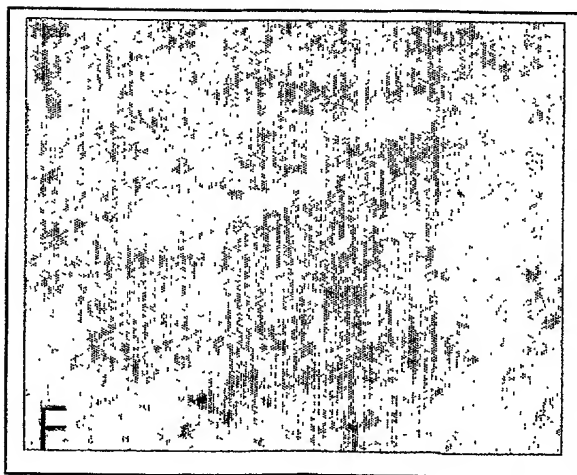


Figure 1F

20250415 09:00:00

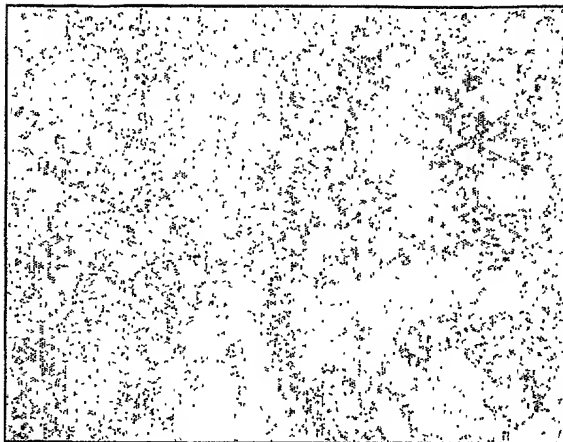


Figure 2A

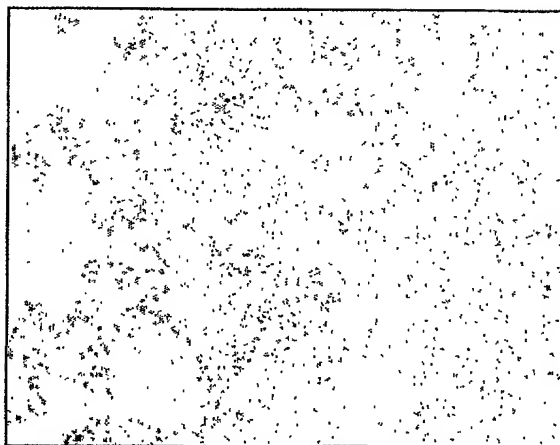


Figure 2B

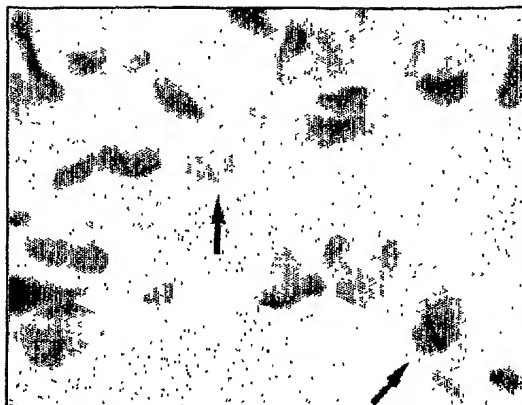


Figure 3A

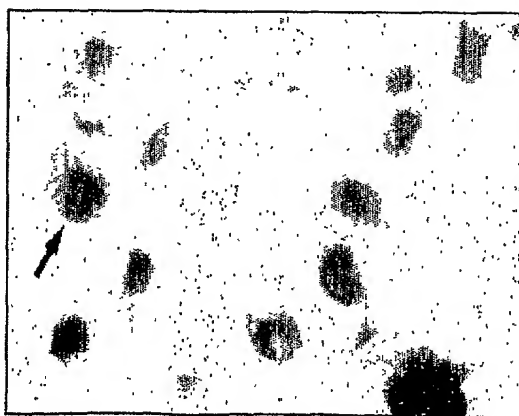


Figure 3B

201050 47698001

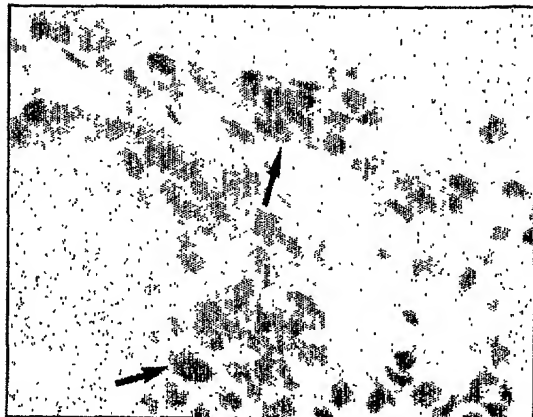


Figure 4A

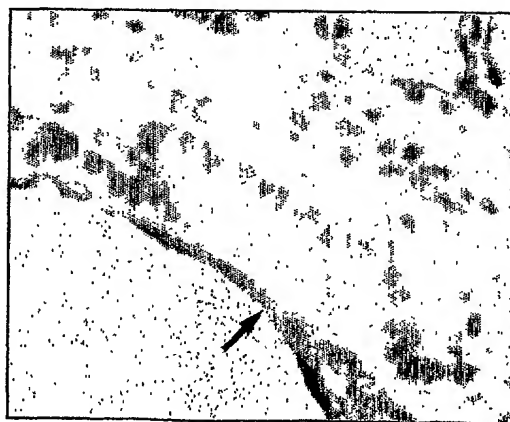


Figure 4B

20140516 085410

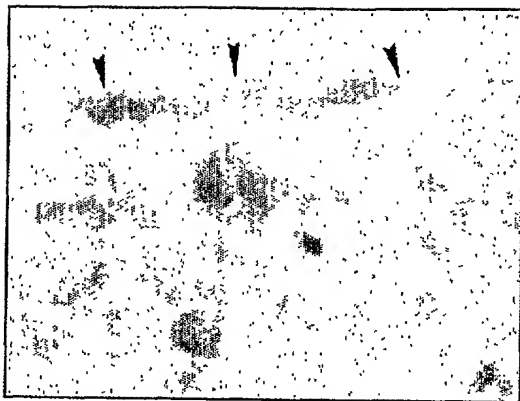


Figure 5A



Figure 5B

201304160001

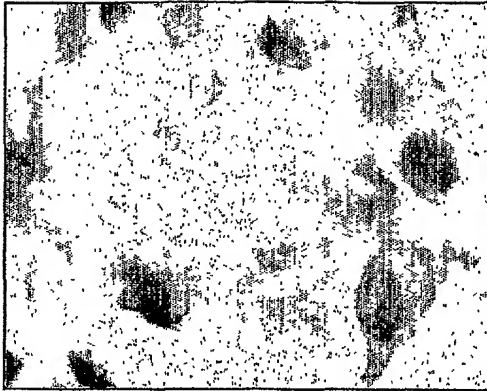


Figure 6A

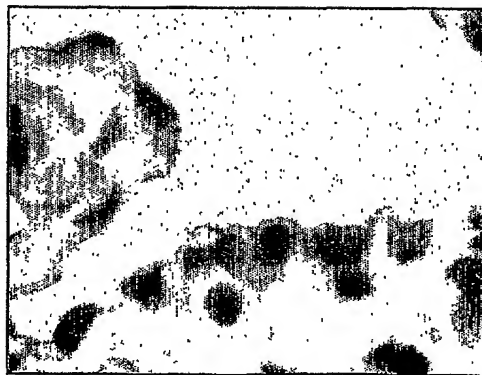


Figure 6B

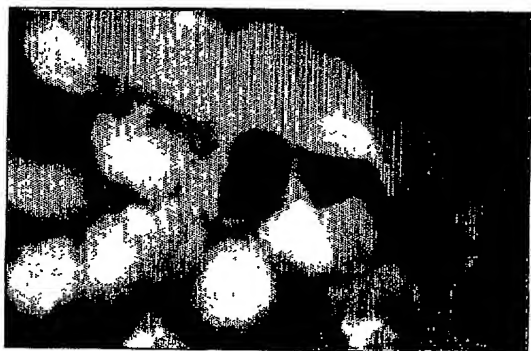


Figure 7A



Figure 7B



Figure 8A



Figure 8B

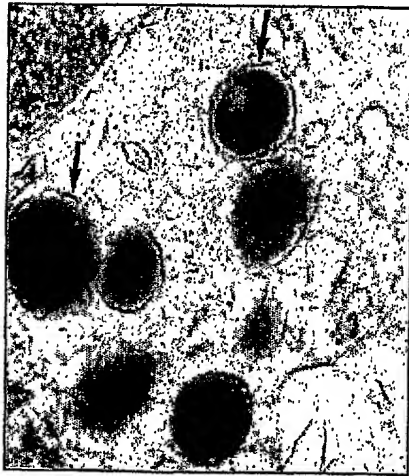
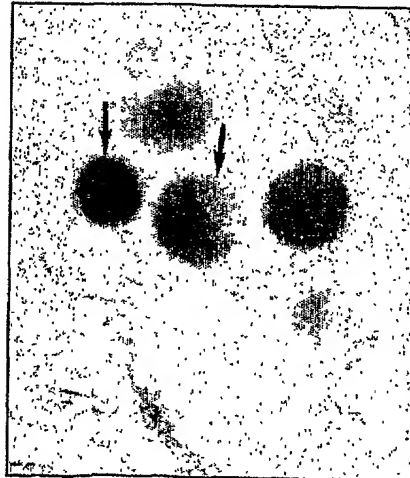


Figure 9A

Figure 9B



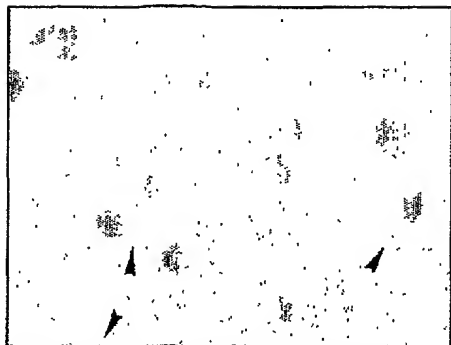


Figure 10A

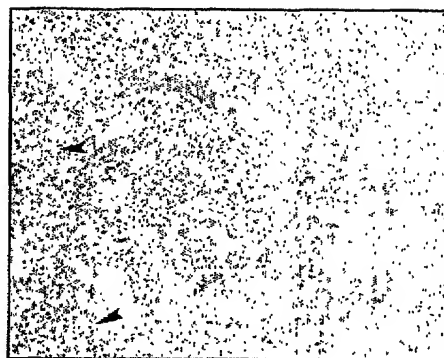


Figure 10B

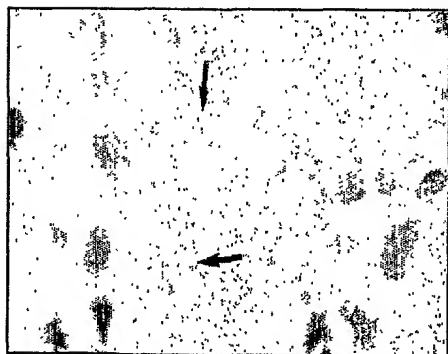


Figure 11A

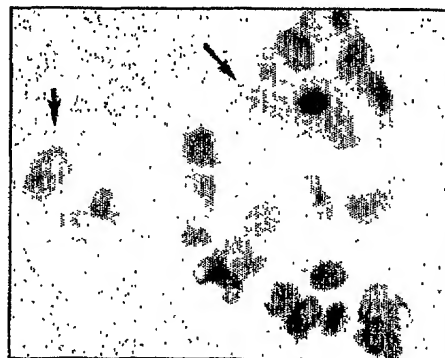


Figure 11B

1008643 1000000



Figure 12A

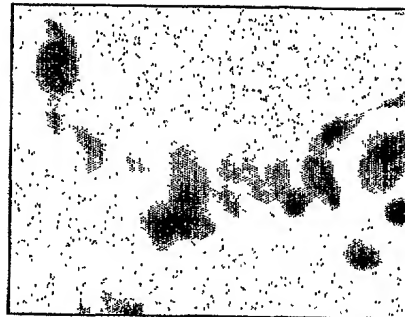


Figure 12B

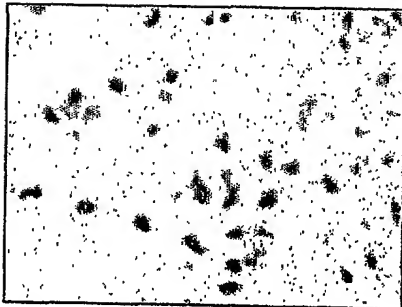


Figure 13A

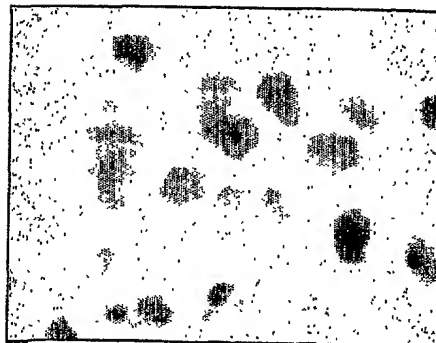
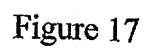
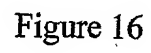
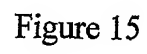
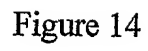


Figure 13B

100864 030100



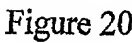
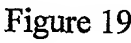
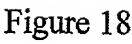




Figure 21

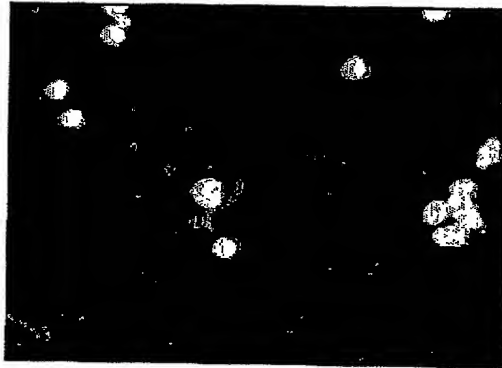


Figure 22

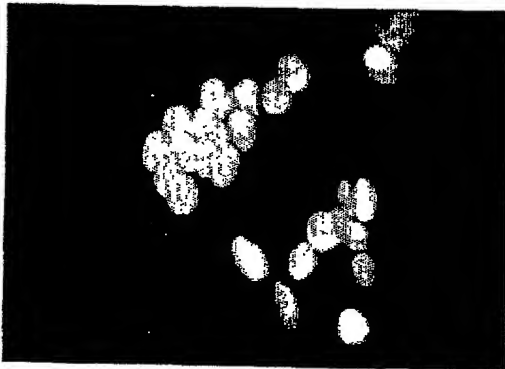


Figure 23

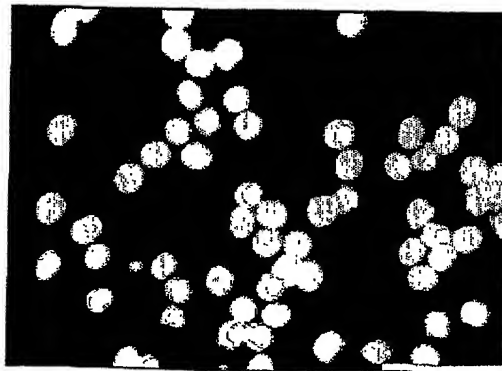


Figure 24

100894 469800

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gaaaagggcg	gcaaagtcac	cgagcgggtt	gtccactcgt	tccgcctccc	cgcccttggt	180
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tccctcattg	atacggtggc	gaagtacagc	gtggacgatg	gggagacgtg	ggagacccaa	300
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SEQ. NO.1

Figure 25

Met	Gly	Ser	Ser	His	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser	His
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Met	Ala	Pro	Gly	Ser	Ser	Arg	Val	Glu	Leu	Phe	Lys	Arg	Gln	Ser	Ser	Lys	Val	Pro	Phe
				25					30					35					40
Glu	Lys	Gly	Gly	Lys	Val	Thr	Glu	Arg	Val	Val	His	Ser	Phe	Arg	Leu	Pro	Ala	Leu	Val
				45					50					55					60
Asn	Val	Asp	Gly	Val	Met	Val	Ala	Ile	Ala	Asp	Ala	Arg	Tyr	Glu	Thr	Ser	Asn	Asp	Asn
				65					70					75					80
Ser	Leu	Ile	Asp	Thr	Val	Ala	Lys	Tyr	Ser	Val	Asp	Asp	Gly	Glu	Thr	Trp	Glu	Thr	Gln
				85					90					95					100
Ile	Ala	Ile	Lys	Asn	Ser	Arg	Ala	Ser	Ser	Val	Ser	Arg	Val	Val	Asp	Pro	Thr	Val	Ile
				105					110					115					120
Val	Lys	Gly	Asn	Lys	Leu	Tyr	Val	Leu	Val	Gly	Ser	Tyr	Asn	Ser	Ser	Arg	Ser	Tyr	Trp
				125					130					135					140
Thr	Ser	His	Gly	Asp	Ala	Arg	Asp	Trp	Asp	Ile	Leu	Leu	Ala	Val	Gly	Glu	Val	Thr	Lys
				145					150					155					160
Ser	Thr	Ala	Gly	Gly	Lys	Ile	Thr	Ala	Ser	Ile	Lys	Trp	Gly	Ser	Pro	Val	Ser	Leu	Lys
				165					170					175					180
Glu	Phe	Phe	Pro	Ala	Glu	Met	Glu	Gly	Met	His	Thr	Asn	Gln	Phe	Leu	Gly	Gly	Ala	Gly
				185					190					195					200
Val	Ala	Ile	Val	Ala	Ser	Asn	Gly	Asn	Leu	Val	Tyr	Pro	Val	Gln	Val	Thr	Asn	Lys	Lys
				205					210					215					220
Lys	Gln	Val	Phe	Ser	Lys	Ile	Phe	Tyr	Ser	Glu	Asp	Glu	Gly	Lys	Thr	Trp	Lys	Phe	Gly
				225					230					235					240
Glu	Gly	Arg	Ser	Asp	Phe	Gly	Cys	Ser	Glu	Pro	Val	Ala	Leu	Glu	Trp	Glu	Gly	Lys	Leu
				245					250					255					260
Ile	Ile	Asn	Thr	Arg	Val	Asp	Tyr	Arg	Arg	Arg	Leu	Val	Tyr	Glu	Ser	Ser	Asp	Met	Gly
				265					270					275					280
Asn	Ser	Trp	Val	Glu	Ala	Val	Gly	Thr	Leu	Ser	Arg	Val	Trp	Gly	Pro	Ser	Pro	Lys	Ser
				285					290					295					300
Asn	Gln	Pro	Gly	Ser	Gln	Ser	Ser	Phe	Thr	Ala	Val	Thr	Ile	Glu	Gly	Met	Arg	Val	Met
				305					310					315					320
Leu	Phe	Thr	His	Pro	Leu	Asn	Phe	Lys	Gly	Arg	Trp	Leu	Arg	Asp	Arg	Leu	Asn	Leu	Trp
				325					330					335					340
Leu	Thr	Asp	Asn	Gln	Arg	Ile	Tyr	Asn	Val	Gly	Gln	Val	Ser	Ile	Gly	Asp	Glu	Asn	Ser
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Ala	Tyr	Ser	Ser	Val	Leu	Tyr	Lys	Asp	Asp	Lys	Leu	Tyr	Cys	Leu	His	Glu	Ile	Asn	Ser
				365					370					375					380
Asn	Glu	Val	Tyr	Ser	Leu	Val	Phe	Ala	Arg	Leu	Val	Gly	Glu	Leu	Arg	Ile	Ile	Lys	Ser
				385					390					395					400
Val	Leu	Gln	Ser	Trp	Lys	Asn	Trp	Asp	Ser	His	Leu	Ser	Ser	Ile	Cys	Thr	Pro	Ala	Asp
				405					410					415					420
Pro	Ala	Ala	Ser	Ser	Ser	Glu	Arg	Gly	Cys	Gly	Pro	Ala	Val	Thr	Thr	Val	Gly	Leu	Val
				425					430					435					440
Gly	Phe	Leu	Ser	His	Ser	Ala	Thr	Lys	Thr	Glu	Trp	Glu	Asp	Ala	Tyr	Arg	Cys	Val	Asn
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Ala	Ser	Thr	Ala	Asn	Ala	Glu	Arg	Val	Pro	Asn	Gly	Leu	Lys	Phe	Ala	Gly	Val	Gly	Gly
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Ala	Phe	Thr	Leu	Val	Ala	Ser	Val	Thr	Ile	His	Glu	Val	Pro	Ser	Val	Ala	Ser	Pro	Leu
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Leu	Gly	Ala	Ser	Leu	Asp	Ser	Ser	Gly	Gly	Lys	Lys	Leu	Leu	Gly	Leu	Ser	Tyr	Asp	Glu
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Lys	His	Gln	Trp	Gln	Pro	Ile	Tyr	Gly	Ser	Thr	Pro	Val	Thr	Pro	Thr	Gly	Ser	Trp	Glu
				545					550					555					560
Met	Gly	Lys	Arg	Tyr	His	Val	Val	Leu	Thr	Met	Ala	Asn	Lys	Ile	Gly	Ser	Val	Tyr	Ile
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Asp	Gly	Glu	Pro	Leu	Glu	Gly	Ser	Gly	Gln	Thr	Val	Val	Pro	Asp	Gly	Arg	Thr	Pro	Asp
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Ile	Ser	His	Phe	Tyr	Val	Gly	Gly	Tyr	Gly	Arg	Ser	Asp	Met	Pro	Thr	Ile	Ser	His	Val
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Thr	Val	Asn	Asn	Val	Leu	Leu	Tyr	Asn	Arg	Gln	Leu	Asn	Ala	Glu	Glu	Ile	Arg	Thr	Leu
				625					630					635					640
Phe	Leu	Ser	Gln	Asp	Leu	Ile	Gly	Thr	Glu	Ala	His	Met	Gly	Ser	Ser	Ser	Gly	Ser	Ser
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Glu	Arg	Ser	Thr	Pro	Gly	Ser	Gly	Cys											
				665															

SEQ. NO.2

Figure 26